

**Table 1.** Significant biological process associated with genes (with the highest depth of coverage) close to the candidate regions affecting on milk yield

| Term ID    | Term Name                                                            | p-Value (adj)      | Gene Name                          |
|------------|----------------------------------------------------------------------|--------------------|------------------------------------|
| GO:0048167 | regulation of synaptic plasticity                                    | 0.0469375676979094 | ARC,ADGRB1                         |
| GO:1901741 | positive regulation of myoblast fusion                               | 0.0469375676979094 | ADGRB1                             |
| GO:1901739 | regulation of myoblast fusion                                        | 0.0469375676979094 | ADGRB1                             |
| GO:1900452 | regulation of long-term synaptic depression                          | 0.0469375676979094 | ARC                                |
| GO:0140239 | postsynaptic endocytosis                                             | 0.0469375676979094 | ARC                                |
| GO:0099177 | regulation of trans-synaptic signaling                               | 0.0469375676979094 | ARC,ADGRB1                         |
| GO:0099149 | regulation of postsynaptic neurotransmitter receptor internalization | 0.0469375676979094 | ARC                                |
| GO:0098884 | postsynaptic neurotransmitter receptor internalization               | 0.0469375676979094 | ARC                                |
| GO:0065008 | regulation of biological quality                                     | 0.0469375676979094 | ARC,ADGRB1,PTK2,ENSBTAG00000004596 |
| GO:0050804 | modulation of chemical synaptic transmission                         | 0.0469375676979094 | ARC,ADGRB1                         |
| GO:0043652 | engulfment of apoptotic cell                                         | 0.0469375676979094 | ADGRB1                             |
| GO:0034650 | cortisol metabolic process                                           | 0.0469375676979094 | ENSBTAG00000004596                 |
| GO:1903428 | positive regulation of reactive oxygen species biosynthetic process  | 0.0469375676979094 | ADGRB1                             |
| GO:0032342 | aldosterone biosynthetic process                                     | 0.0469375676979094 | ENSBTAG00000004596                 |
| GO:0006705 | mineralocorticoid biosynthetic process                               | 0.0469375676979094 | ENSBTAG00000004596                 |
| GO:0007172 | signal complex assembly                                              | 0.0469375676979094 | PTK2                               |
| GO:0034309 | primary alcohol biosynthetic process                                 | 0.0469375676979094 | ENSBTAG00000004596                 |
| GO:0016192 | vesicle-mediated transport                                           | 0.0469375676979094 | ARC,ADGRB1,TSNARE1                 |
| GO:0008212 | mineralocorticoid metabolic process                                  | 0.0469375676979094 | ENSBTAG00000004596                 |
| GO:0032341 | aldosterone metabolic process                                        | 0.0469375676979094 | ENSBTAG00000004596                 |
| GO:0016477 | cell migration                                                       | 0.0469375676979094 | ARC,ADGRB1,PTK2                    |
| GO:0060142 | regulation of syncytium formation by plasma membrane fusion          | 0.0474044018931508 | ADGRB1                             |
| GO:0060143 | positive regulation of syncytium formation by plasma membrane fusion | 0.0474044018931508 | ADGRB1                             |
| GO:0048870 | cell motility                                                        | 0.0474044018931508 | ARC,ADGRB1,PTK2                    |
| GO:1902644 | tertiary alcohol metabolic process                                   | 0.0474044018931508 | ENSBTAG00000004596                 |
| GO:0008211 | glucocorticoid metabolic process                                     | 0.0474044018931508 | ENSBTAG00000004596                 |
| GO:0046184 | aldehyde biosynthetic process                                        | 0.0474044018931508 | ENSBTAG00000004596                 |
| GO:0099590 | neurotransmitter receptor internalization                            | 0.0474044018931508 | ARC                                |
| GO:0120255 | olefinic compound biosynthetic process                               | 0.0474044018931508 | ENSBTAG00000004596                 |
| GO:0006910 | phagocytosis, recognition                                            | 0.0474044018931508 | ADGRB1                             |
| GO:0006704 | glucocorticoid biosynthetic process                                  | 0.0474044018931508 | ENSBTAG00000004596                 |
| GO:0006700 | C21-steroid hormone biosynthetic process                             | 0.0474044018931508 | ENSBTAG00000004596                 |
| GO:0001525 | angiogenesis                                                         | 0.0474044018931508 | ADGRB1,PTK2                        |
| GO:0060292 | long-term synaptic depression                                        | 0.0485602745820948 | ARC                                |

**Table 2.** Significant biological processes associated with genes (with the highest depth of coverage) close to the candidate regions affecting environmental stress tolerance

| Term ID    | Term Name                                                 | p-Value (adj)      | Gene Name |
|------------|-----------------------------------------------------------|--------------------|-----------|
| GO:0009756 | carbohydrate mediated signaling                           | 0.0496296163797798 | SMARCB1   |
| GO:0009757 | hexose mediated signaling                                 | 0.0496296163797798 | SMARCB1   |
| GO:0010182 | sugar mediated signaling pathway                          | 0.0496296163797798 | SMARCB1   |
| GO:0010255 | glucose mediated signaling pathway                        | 0.0496296163797798 | SMARCB1   |
| GO:0021999 | neural plate anterior/posterior regionalization           | 0.0496296163797798 | CELSR2    |
| GO:0033326 | cerebrospinal fluid secretion                             | 0.0496296163797798 | CELSR2    |
| GO:0060896 | neural plate pattern specification                        | 0.0496296163797798 | CELSR2    |
| GO:0060897 | neural plate regionalization                              | 0.0496296163797798 | CELSR2    |
| GO:1902659 | regulation of glucose mediated signaling pathway          | 0.0496296163797798 | SMARCB1   |
| GO:1902661 | positive regulation of glucose mediated signaling pathway | 0.0496296163797798 | SMARCB1   |